CLAIMS

We claim:

1. A method of isolating one strand of a double-stranded target nucleic acid, comprising:

(i) contacting a double-stranded target nucleic acid comprising a first strand and a second strand with a competitor oligo capable of hybridizing to the first strand under conditions in which the first strand dissociates from the second strand and hybridizes with the competitor oligo to form a first-strand:competitor oligo heterduplex; and

(ii) isolating the heteroduplex or the dissociated second strand.

2. A method of isolating one strand of a double-stranded target nucleic acid, comprising:

(i) dissociating the double-stranded target nucleic acid into a first strand and a second strand;

(ii) contacting the dissociated target nucleic acid with a competitor oligo capable of hybridizing to the first strand under conditions which favor first-strand:competitor oligo heteroduplex formation and disfavor reannealing of the first and second strands; and

(iii) isolating the heteroduplex or the dissociated second strand.

3. The method of Claim 1 or 2 in which in step (ii) the heteroduplex is isolated.

4. The method of Claim 3 further comprising the step of dissociating the heteroduplex and isolating the first strand.

5. The method of Claim 1 or 2 in which in step (ii) the second strand is isolated.

6. The method of Claim 1 or 2 in which the double-stranded target nucleic acid is a double-stranded DNA.

7. The method of Claim 1 or 2 in which the double-stranded target nucleic acid is a double-stranded DNA/RNA hybrid duplex.

8. The method of Claim 1 or 2 in which the competitor oligo is composed of between 7 and 40 nucleobases.

9. The method of Claim 1 or 2 in which the double-stranded target nucleic acid has the formula:

TAIL 1---SEQUENCE---TAIL 2
TAIL 1'--SEQUENCE'--TAIL 2'

wherein:

TAIL 1 represents a first tail nucleobase sequence;
SEQUENCE represents a target nucleobase sequence;
TAIL 2 represents a second tail nucleobase sequence;
TAIL 1' represents a nucleobase sequence that is complementary to TAIL 1;
SEQUENCE' represents a nucleobase sequence that is complementary to SEQUENCE; and
TAIL 2' represents a nucleobase sequence that is complementary to TAIL 2.

10. The method of Claim 9 in which a portion of the competitor oligo is capable of hybridizing to TAIL 1 and another portion of the competitor oligo is capable of hybridizing to TAIL 2.

11. The method of Claim 9 in which a portion of the competitor oligo is capable of hybridizing to TAIL 1' and another portion of the competitor oligo is capable of hybridizing to TAIL 2'.

12. The method of Claim 9 in which TAIL 1 and TAIL 2 comprise non-standard synthetic nucleobases.

13. The method of Claim 9 in which TAIL 1 and TAIL 2 are not complementary to one another.

14. The method of Claim 1 or 2, in which the competitor oligo includes a capture moiety.

15. The method of Claim 14, in which the capture moiety is one member of a pair of molecules that specifically bind to each other.

16. The method of Claim 15, in which the capture moiety is biotin.

17. The method of Claim 14, in which the moiety is a solid support.

18. The method of Claim 17, in which the solid support is magnetic.

19. The method of Claim 14 in which the capture moiety is a capture sequence.

20. The method of Claim 16 in which the capture moiety is a charged group.

21. The method of Claim 1 or 2 in which the competitor oligo is capable of hybridizing to only the first or the second strand of the double-stranded target nucleic acid.

22. The method of Claim 1 or 2 in which the contacting step is carried out at a cationic strength in the range of 0 to 10 mM, a pH in the range of 6 to 8, and a temperature in the range of 20 to 40°C.

23. The method of Claim 1 or 2 in which the competitor oligo is a PNA and optionally includes from 1 to 4 positively charged nucleobase interlinkages.

24. The method of Claim 1 or 2 in which the competitor oligo comprises non-standard synthetic nucleobases.

25. A method of isolating one strand of a double-stranded target nucleic acid, comprising the steps of:

(i) dissociating the double-stranded target nucleic acid into a first strand and a second strand;

(ii) contacting the dissociated target nucleic acid with a competitor oligo capable of hybridizing to only the first strand under conditions which kinetically favor competitor oligo first-strand hybrid formation and kinetically disfavor reannealing of the first and second strands, said competitor oligo being conjugated with a moiety that facilitates capture of competitor oligo:first-strand hybrids; and

(iii) capturing the competitor oligo:first strand hybrid.

26. The method of Claim 25 wherein the competitor oligo is a PNA.